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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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ALIGNMENTS

AXO16311
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DEFINITION
Sequence 14 from Patent W09949046.
ACCESSION
AXO16311
VERSION
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VERSION
AXO16311.1 GI:10041874

KEYWORDS
SOURCE
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AUTHORS
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PATENTY
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Endrophyta; Endr

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Whitelaw, C.A., Paul, W., Jenkins, E.S., Taylor, V.M. and Roberts, J.A.
                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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ANNGEEAVIIHRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNE
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/db_xref="taxon:3708"
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TCACCTACACGTGTATTTGACACAAAAATCTGCATTTGTTGTGATATAGGGTTTCTCATA
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AX016324
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1 (bases 1 to 818)
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SVADDEERKAFMEAGLNHCLEKPLTKAKIFPLISHLEDA"
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/db_xref="GI:10041880"
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1 (bases 1 to 576)

1 (bases 1 to 576)

Roberts, J. A., Wyatt, P. and Whitelaw, C. Signal transduction protein involved in plant dehiscence Patent: WO 9949046-A 25 30-SEP-1999; ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB); WHITELAW CATHERINE (GB)
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-CTTTATCGTCCGTGATATATATATCATGTAAGTTGTTGCTTTAAGCTTA 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prediction programs including GRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefider (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/netpgene/obsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/rdb/ac/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity are named as 'unknown' proteins. Genes without protein programs over most of their length are annotated as 'nypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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Submitted (24-CAN-2001) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Jan 24, 2001 this sequence version replaced gi:12280893.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC clone T6K12 is from Arabidopsis chromosome III and is near the molecular marker mi172.
The orientation of the sequence is from SP6 to T7 end of the BAC
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Submitted (08-DEC-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 110804)
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                                               complement(join(<1. .100,188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<7363. .8357,8709. .9180,9625. .9825,9900. .10193,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF26777.1"
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//tb_xref="G1:6721145
//tb_xref=|
//t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPGMYLQGSSKLGIGVRNDVAKSKYIVDSSQRYVIVAAEYLGKGAVIEPCWLQYMREW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <4235. .6750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mgrlkfacpyleinlisaqdlapvsrnmktysyamintdpmrkl
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yfdgsrkgernsykrdqeasramhrrtnsdqtdlttstndygvktgyvtgnggevyvy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVRKGCFHVLETCLDVRFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRELS I ELNGGEQRKMARVERVERLDQAMI LAGKEEREGEEGGGEERRNNKGGETVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVLLLVRIVWLMVRFVALILDHQRLWLRLRLRKGFTIDRKQRLKRLTKRTQVRYLKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2505, .3566
/gene="T6Kl2.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEGSKVNTGKSLAIVVGGVAALVFVAIFFMFLKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<1. .100,188. .556,813. .1275))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <2505. .>3566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="T6K12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y="(GGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4346,5141. .6732)
12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6750)
                                                                                                                                                                                                                                                                                         .9825,9900 .10193,
.11135,11282 .11403,
.12663,12753 .12827,
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Query Match
Best Local Similarity
Matches 454; Conserv
                                                                          30007 AATCGAAGATGGCAACAAAATCCACCGGAGGTACCGAGAAAACCAAGTCGATAGAAGTGA 30066
                                                                                                                    12 AATCGAAGATGGCAACAAAATCCATGGGAGATATCGAGAAAATAAAGAAGAAGAACTA---- 67
------AACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATG 113
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESKKLORDLONRIŘKMKKŘGEEKLĚVOKTPEGEAVKGFPEAEVKWMTGEKEVVVPKA
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KSRWEMDPMA VPYAVSSKLUDSAR IRHDYA VKYVALKODDKEPYVDI KEYPEMLFEKRÉ
OTVLEKIRNI NDD IMMA VVFPVI EFI I PYQLAR LEGAMPEEL ELEGIVOSTWILOWOSE
OTVLEKIRNI NDD IMMA VVFPVI EFI I PYQLAR LEGAMPEEL ELEGIVOSTWILOWOSE
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FURNKSYSTY KKRRIKOK KRAGIDPIKTAFDRMKRVKNPPILGKOPERSINE
VVAFLOMFKAPOEMGAKAPROLLAVI I I TVEDEDLE FOVENCKYNFT KOODHESE I NOLLVE
UNGEGSANVERLFOTARDLAVI I TVEDEDLE FOVENCK FVHIKODHESE I NOLLVE
DGFEKKODGVUMATTENHKOLDEALKRONDEN SAMPROLENGEREILHNAAEETM
DET HUT UNDER VEGSTER VEGSTER SAMPROLENGEREILHNAAEETM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(16278. .17012)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to trypsin inhibitor:ISOTYPE=a GB:737210; contains Pfam profile: PF00197 trypsin and protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<16278. .>17012)
/gene="T6K12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGDGPDYLTTISLSNDYPIYRLLSKKFSGEMEIYFYKNLTMG"
complement(<16278. .>17012)
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/translation="MKTFENMLISLILLVAITTTSGVVEGNYVVYDGEGDQVKPNVPYY
ISFMTSDYNMWICRKKWRSNDPNSCPQQPLMVTHPNMAAPTFVMFVLSKKSETVVRES
AKLKIKTVDPRPCGESGFWRYVQRTSSEGEVVLNGSESTSDNASTFAIEQTNEYYKFT
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/gene="r6K12.5"
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/gene="f6K12.5"

/note="sinilar to trypsin inhibitor:ISOTYPE=a GB:737210;

contains Pfam profile: PF00197 trypsin and protease
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/gene="T6K12.5"
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DSPAVYYATNAVSALSWGNNHEYEMAGKVEKIYDLAYEKAKGMLLKNRRVLEKITEEL
LEFEILTHKALSRSFLDVGDPPETALLSAPT"
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HIVPFWLRKTKVAKTMGKMLVNHLGLNLTKDDLENVVDLMEPYGQISNGIELLNPTVD
WTRETKFPHAVMAAGRALITLLIPNFDVVENLWLEPSSWEGIGCTKITKVTSGGSAIG
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EYNKIWERIDEIDDIILKKETTTLSFGVRELIFIERECVELVKSFNRELNOKSFESVP
ESSITKLSRSEIKQELVNAQRKELEQMILPNVLELEEVDPFFDRDSVDFSLRIKKRLE
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SNNKSRKIVPIRGCFGFSGSFLRSKQSBYGSEAVSESLRLCGSDELVLSSEYNSAKT
RESVIQFVTRPLVYALFCIAIGLSFIRSFQAPJAVPEVSDVIWKKKERRVRKEVVL
KAYDHEFSDYTRRLLETYSVLLKTIEIVRKENGEVAEVGAALDAVKVEKEKLQKEIMS
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/codon_start=1
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/codon_start=1
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/gene="T6K12.7"
                                                                                                                                                                                                                            28.3%; Score 171.2; DB 8; 60.5%; Pred. No. 1e-31; tive 0; Mismatches 133;
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CDS	EATURES Source	TITLE JOURNAL	RENCE	URCE ORGANISM	VERSION KEYWORDS	DEFINITION ACCESSION	LT 6 6320	30727	569	30667	522	30607	465		411	87	351	27	291	30367	07	253	30247	234	30187	174	30127	114	30067
:3708" protein	Location/Qualifiers 11716 /organism="Brassica	KODEITS, J.A., WYALT, F. and WHITELAW, C. Signal transduction protein involved in plant dehiscence Patent: WO 9949046-A 23 30-SEP-1999; ROBERTS JEREMY ALAN (GB); BIOGEMWA UK LTD (GB); WYATT PAUL (GB); WHITELAW CATHERINE (GB)	a; viridipiancae; streptopny phyta; Magnoliophyta; eudico ; eurosids II; Brassicales; B ss 1 to 1716)		AX016320.1 GI:10041876	9949046.	1716 b	TGGCTAATAAATATTAAAATAAGGTTTTC 30756	TTAAAT	ATATOTATGTTTGATTTATTTTTTTATCGTCCGAGGTAAAATCATGCAAGTCATTTCTTT 30726	AGGGTTCTTTATCGTCCGTGATATAATCATGTAAGTTGTTGCTTT 568	AAATCACCTACACGTGTATTTGACACAAAAAATCTGCATTTGTTGATATAGGGTTTCTC 30666	ATAACGICTAAGIGIGIAIGIAIGCATAGATACIIGCAIGIGIGIGITTIIAGAAITI	ATGTATCTATATTTTCAATCATG 30	ACCAACTCATGGATGCTTGATGGATATATTTTTATATTATGGAAACACACATA 464	TGGGCTCAACCATTGCTTGGAAAAACCCTTAACCAAGGCCAAGATCTTCCCGCTCATTA 30	CTGGACITAACCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTA 410		TGATTGTTGGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGGCTTTCATGGAAG 350	TGTTCTTTGTTGATTTAATTTAGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAA 290	A 30	252	GGATGGAGTT	CCGAGAGGGATGGTGTTTC252	GTGACGGCGAAGCATCTTTCGACCTTATTCTAATGGATAAGGAAAT	TAATCATCCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGC 233	AGATGATCAAAAACGATCGGAGGAATTTCTCAGACTGCAAAGAATGGCGAGGAGGCAG 30186	CATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAG	AGAAGAAACTAATCAACGTGTTGATCGTCGATGATGATCCATTAAACCGTAGACTCCACG 30126

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                      GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAA 360
                                                                                           GGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGG
                                                                                                                  CCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAG 240
                                                                                                                                                                 CAGTGAACATCCACCGCGACGGC 1710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGAGAATATCATCAAATCGATCGGTGGAATTTCACAGACGGCTAAGAACGGTGAGGAGG 1687
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                                                                     1 Similarity
33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified
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/db_xref="GI:10041877"
/translation="MATTSTSTGDIKKTKSVEVKKKLNVLIVDDDTVIRKLHENIIKS
IGGISQTAKNGEEAVNHHRDGNA"
256 c 264 g 576 t 16 others
                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
1491 c 1486 g
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1. .7218
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TTTCGATTTAATTATCATGGATAACCATATGCCTGTAATGGACGGTATTTTAGCCACAAA 2946
                                                             TTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAGGGATGGTGTTTCGACAACTAA 261
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Vibrio fischeri RscS (rscS) gene,
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Vibrio fischeri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Visick, K.L. and S. Direct Submission
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/product="Rsc6"
/product="Rsc
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KRPSKYKLSDDALTEAEIKLTSIQDICGTDSEIICVFLQSFIDTSEENITEIITAFER
KDIKSIRFYAHSIKGMASNESASRLIKIATSIELCAKKKNMPKLEDVQQLINLLKINI
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/db_xref="taxon:668"
782. .3565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 19, 2001 this sequence version replaced gi:17384505.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. EMBL; SW:,
SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
thttp://www.sanger.ac.uk/Projects/C.elegans/wormpen_This_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCAAGGACAAGATCATCCCTCTCATTAACCAACTCATGGATGC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9 constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/BGP/Chr9
RP11-1771B is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                    RP11-17718 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-515J13 is at 109753 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-DEC-2001) Wellcome Trust Sanger Institute, Hinxton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                            /clone_lib="RPCI-11.1"
19899 c 20215 g 37062
                                                                                                                                                                      /chromosome="9"
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                              /clone="RP11-17718"
Score 51.4;
Pred. No. 0.
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DB 9;
.021;
                     Length 111752;
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TAAATTTGTATTTATTGCACTGAGGTAAAAAATATTCTGTATATCAGCTCCC
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Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,
Koonin, E. V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,
Koonin, E. V., Shallom, S., Mason, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,
Smith, H.O., Fraser, C.M., Hoffman, S.L. et al.
Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
AE001420 AE001362
AE001420.1 GI:3845287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-NOV-1998) The Institute for Genomic Medical Center Drive, Rockville, MD 20814, USA
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                                                                                                                                                                                                                     complement(4112.
/gene-"PFB0835c"
/translation="mikyinkskalllrkmstvknmsksnqltkeifmalkektsllq
/keklyiefyebhlclskletscoletktelmyksridtnyvblkvybekgegskgtnnom
lnnndxtsfstdnokgfinketeggeekknetmanyebhkyvbekgyglulpybyk
Vefykhiielidslaadvvyrhsigvykrndkynfvtvlfnnlktyeknvfhhefsfa
                                                                                                                                                                                                                                                                     complement(4112.
/gene="PFB0835c"
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/tzanslation="MPKXERNGGRSKHNRGHVNPLRCSNCGRCVPKDKAIKRFNIRNI
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                                                                                             /product="hypothetical protein"
/protein_id="AAC71956.1"
/db_xref="GI:3845289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Plasmodium
/db_xref="taxon:5833"
                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                             /note="predicted by GlimmerM"
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GCATTATTTTGATGAACGATGTCATCCAACCTTTTTGGTCGGTACTTTTCAACCCACGGA 7545
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SRCSCYRFQSIPINIKKEKLLYICQNENIDIVDDALEKIIET/TEGDLERAVSIIQLCS
CINTKITLNSYLDVSGLPSDNIVYKIIDACKKKDLKLVEKTYQDIIEDGFDVAYIFKS
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NSWQNEXYKQIKSLCSHIKDVQSLFNYKEVKSKTLHPNDMEILSNPFKKYQTQNLGYI
KNINEYTNIYUNEQNBLVQNSMDNILTIFDSILNLNDFSFHAGKVQYACKDTYVQSNH
FISSEEXNIHNETFGGHLAYLSFCHAWVVIKKELPKFILMQINSIQYILPVFVNSEVL
YKGKVVYSDQHSIQVHVATYCFDFKKSAYYLTTICDMSFENNSDISFVPQSQEEFKLY
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FLLCLLYITLNGKDKFIIFNMLYSIIYFVINAIYHGLNYPLMGTLNLFFSTYLLELYI
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Best Local Similarity
Matches 114; Conserv
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Fragment Nam
1-193488
Birren B., Lin:
"Homo sapiens of
Unpublished.
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PFMAL13P2_1
PFMAL13P2_2
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                                                            Eukaryota;
Eutheria;
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25 unordered
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                                                                                                HTG; HTGS_DRAFT; HTGS_PHASE1
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28-MAY-2000
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                                                                                                                                                                                                                                                                                                                             GCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAATCATGTAAGT 559
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          Linton L., Nusbaum C., ens chromosome 4, clone
                                                                      Metazoa;
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                                                           Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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          Lander E.; RP11-402C9";
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dve-terminator B1g Dve; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 1877768 bases at least Q40
Consensus quality: 187917 bases at least Q20
Consensus quality: 187917 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 191088; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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1-193488
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1339: contig of 1339 bp in length
1340 1439: gap of
100 bp
1440 2663: contig of 1224 bp in length
2664 2763: gap of
2764 4211: contig of 1244 bp in length
4212 4311: gap of
4312 5618: contig of 1307 bp in length
5719 6795: contig of 1307 bp in length
6796 6895: gap of
6896 9287: contig of 1077 bp in length
9288 9387: gap of
1178: contig of 2392 bp in length
1179 1178: contig of 1791 bp in length
11374 13748: contig of 2470 bp in length
13749 13848: gap of
15940 16039: gap of
16040 17849: contig of 2091 bp in length
15940 16039: gap of
1100 bp
112849: contig of 2470 bp in length
15940 16039: gap of
100 bp
11809: contig of 100 bp
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**Reterston,R.H.*

Direct Submission

Submitted (25-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 8, 2002 this sequence version replaced gi:18370048.
      Sequencing vector: M13; 35%
Sequencing vector: plasmid; 65%
                                                                                      Drafting center: WIBR
                                                                                                      Center project name:
                                                                                                                                            Contact: submissions@watson.wustl.
                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
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1 (bases 1 to 198509)

Waterston, R.H.
                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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159694. .193488
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73228. .82813
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136476. .159593
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121749. .136375
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94982. .107947
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Consensus quality: 195481 bases at least (
Insert size: 179000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 179000; agarose-fp
Insert size: 197809; sum-of-contigs
Quality coverage: 13.78 in Q20 bases; agarose-fp
Quality coverage: 13.76 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this greence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                    59384
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be preserved.
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13180
13280
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13280. .198509
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38737 c 39643 g 60041 t
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/chromosome="4"
/clone="RP11-402C9"
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10678. .13179
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1737. .6279
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56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1407: contig of 1407 bp in length
1507: gap of unknown length
2836: contig of 1329 bp in length
4936: gap of unknown length
4636: contig of 1700 bp in length
4736: gap of unknown length
6279: contig of 1543 bp in length
6379: gap of unknown length
7570: contig of 1191 bp in length
7570: gap of unknown length
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SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

REFERENCE

AUTHORS TITLE

JOURNAI

RESULT 13 AC108142/c LOCUS

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Matches Query Match Best Local

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REFERENCE AUTHORS

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Gaps

Db 127538 ACATATATTTGTGTATATATACACATATATATGTGTATA 127498

COMMENT TITLE JOURNAL AUTHORS

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Homo sapiens chromosome 3 clone RP11-90B15,
AC099331 AC073441
AC099331.2 GI:18852541
Submitted (09-NOV-2001) Genome Center, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 151498)
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 151498)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saephimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1324)
Roberts, J. A., Wyatt, P. and Whitelaw, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal transduction protein involved in plant dehiscence Patent: WO 9949046-A 29 30-SEP-1999; ROBERTS JEREMY ALAN (GB); BIOGEMMA UK LTD (GB); WYATT PAUL (GB); WHITELAW CATHERINE (GB)
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                                               Kaul,R.K., Olson,M.V., Raymond,C. and Direct Submission
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/db_xref="G1:10041882"
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214 c 182 g 467 t 1 others
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/note="unnamed protein product"
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                                                             Haugen, E.D
                            University of Washington
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Overlapping Sequences: 5': Mapping in pr 3': RP11-613N24 (

Mapping in progress RP11-613N24 (UWGC:bc0491) AC099557

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality - 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

SeqDerMap This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. 6382 512 970 HindIII FngrPrnt <800 6463 SeqDerMap 5474 8580 2067 BglII EngrPrnt 5794 2050 8813 SeqDerMap 6481 8696 ECORI FngrPrnt 6581 <800 ďď

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Search completed: November 7, 2002, 14:05:25 Job time : 2373 secs	Query Match 8.1%; Score 48.8; DB 9; Length 151498; Best Local Similarity 51.9%; Pred. No. 0.09; Matches 110; Conservative 0; Mismatches 102; Indels 0; Gaps 0; 97 379 GTTAACCAAGGACAAGATCACCCTCTCATTAACCAACTCATGGATGG	## 434

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Result
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Brassica response
Arabidopsis thalia
A. thaliana DZZATJ
Arabidopsis thalia
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Brassica response
Brassica napus DZZ
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 Brassica response
                      10-JAN-2000
                                                                   AAZ22977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 1;
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 regulator
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605;

Conservative

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Score 605; DB 20; Pred. No. 3.9e-159; 0; Mismatches 0;

Length Indels

605; 0;

Gaps

0,

Similarity

100.0%;

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A nucleic acid encoding dehiscence, useful for p
                                                                                                                  WPI; 1999-580449/49
                                                                                                                                                                                                                                                                                                                                                                            signal transduction shatter resistance;
   Example 2;
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                                                                                                                                                                                                                                                                                                                                             Brassica napus
                                                                                                                                                                              (BIOG-)
                                                                                                                                                                                BIOGEMMA UK
                                                                                                                                                 Roberts JA,
 Fig
6; 71pp; English
                                                                                                                                                                                                               98GB-0006113
                                                                                                                                                                                                                                                99WO-GB00905
                                                                                                                                                                                                                                                                                                                                                                           protein; dehiscence; male sterile plant; I
oilseed rape; response regulator protein;
                                              g a signal
                                                                                                                                                   Whitelaw
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                                              transduction protein involved in plant shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                              SS
                                                                                                                                                                                                                                                                                                                                                                                          gene;
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The pressequence represents the B. napus DZ2 sequence. Sequence 605 BP; 198 A; 101 C; 140 G; 166 T; 0 other; present o

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                                    GGATGCTTGATGGATATATTTTATTATTGGAAACACACATAATAACGTCTAAGTGTG
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                 50.3%;
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               Wyatt P,
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                                                                                                                                                                                                                                                                                               A. thaliana
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                                                                                                                                                                                                              Arabidopsis thaliana
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                 Roberts JA, Whitelaw C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A nucleic acid encoding dehiscence, useful for r
                                      AAC47939 standard;
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                                                                                                                            CTAATAAAATATTAAAATAAGGTTTTC
                                                                                                                                                            CTTATAAAATATTTAAATAAGGGTTTC
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                                                                                                                                                                                                                                                                                                          ACCTCTTCGATGCTTGATGGATGAAGGCTCATTAATGTATCTATATTTTCAATCATGAAA
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CCGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGA
                                                                                                          TAATCATCACCGTGACGGCGGCTCATCTTTGACCTTATCCTAATGGATAAAGAAATGC
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                                                                             -----ACGTGTTGATCGTCGATGATGATCACTAAACCTTATAATTCATG
                TGATCCTCCACCGTGACGGCGAAGCATCTTTCGACCTTATTCTAATGGATAAGGAAATGC
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Best Local 9
                                                                                                                                                                                                                                                                                        Signal transduction protein; dehiscence; male sterile plant; DZ2B gene; shatter resistance; oilseed rape; response regulator protein; ss.
                                                                                                                                                                                                                                                                                                                                                                 Brassica response regulator protein DZ2B cDNA sequence
  (BIOG-) BIOGEMMA UK LTD
                                                 20-MAR-1998;
                                                                                             22-MAR-1999;
                                                                                                                                              30-SEP-1999
                                                                                                                                                                                           WO9949046-Al
                                                                                                                                                                                                                                            Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ22976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTATAAAATATTTAAATAAGGG
|| |||||||||||
CTAATAAAATATTAAAATAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTTAACCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCCATTAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTTGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTCTTCGATGCTTGATGGATGAAGGCTCATTAATGTATCTATATTTTCAATCATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                              98GB-0006113
                                                                                             99WO-GB00905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sim
Matches 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed trape (Brassica napus). The present sequence represents the B. napus DZ2B cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A nucleic acid encoding a signal transduction protein involved in dehiscence, useful for producing shatter resistant male sterile pl
            AAZ22975;
                                      AAZ22975 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>_</u>
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DB; AAY42652.
                                                                                                                               TAAAATATTTAA
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                                                                                                                                                                                                                                                                                                                 CGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCATGGATGCTTGATGGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGTCGATGATCCACTAAACCTTATAATTCATGAGAAGATCATCAAAGCGATTGGGG
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                                       DNA;
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75.4%;
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Best Local :
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         Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modifiplant cell signalling; modulation; transgenic plant; pathogen; environmental change; development; cell proliferation; different elongation; survival; disease resistance; nutrient metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal transduction shatter resistance;
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                                                                                                                                                                                                                                                                              1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A nucleic acid encoding a signal dehiscence, useful for producing
                                                                           Pinus radiata cell signalling involved polynucleotide SEQ
                                                                                                     27-NOV-2000
                                                                                                                                                                                                                                                                                                                                 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1716 BP; 604 A; 256 C; 264 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus
                                                                                                                                                          AAA79325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                               AAATAAAGAAGAAACTAAACGTGTTGATCGTCGATGATGATGATCACTAAACCTTATAATTC 110
                                                                                                                                                                                                                           CAGTGAACATCCACCGCGACGGC 1710
                                                                                                                                                                                                                                                   CAGTAATCATCCACCGTGACGGC 193
                                                                                                                                                                                                                                                                           AAGTGAAGAAGAAACTTAACGTGTTGATCGTTGATGATGATACAGTAATTCGTAAACTTC 1627
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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oilseed rape; response regulator protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 17.6%;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 106.2; DB 20;
Pred. No. 1.1e-19;
0; Mismatches 23;
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Gaps

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nt; modification; nathogen; growth; differentiation;

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NO:63.

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RESULT 10
AAZ22979
ID AAZ22
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DE A. th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and protein sequences isolated from eucalyptus (Eucalyptus grandis) or the pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynuclectide and protein sequences sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
    A. thaliana DZ2AT3 promoter
                                   10-JAN-2000
                                                                  AAZ22979;
                                                                                             AAZ22979 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1656 BP; 514 A; 283 C; 400 G; 459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 58; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pinus radiata
                                                                                                                                                                         728
                                                                                                                                                                                                      252
                                                                                                                                                                                                                                     671
                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                              132
                                                                                                                                                                                                                                                                                                                                                    551 TCTTGCTCGTGGAAGACACACAAATCAACAGAATAATTTTCGGGAGGGTGCTTCAAAGCC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                72 TGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGATCATCAAAGCGA 131
                                                                                                                                                                                                CGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCA 310
                                                                                                                                                                                                                                                            GCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCCGAGAGGGATGGTTTT
                                                                                                                                                                                                                                                                                         TTAATCTTTACTGTGAAGAAGCTGAGAATGGGAAAGTAGCAGTGGACTATTTCAAGCAGG
                                                                                                                                                                                                                                                                                                                       TTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAATCATCCACCGTGACG 191
                                                                                                                                                                    AGGCAACAAGGCAACTGAGATCAATGGGAGTCAAGACACCCATTGTTGCACTTACAGCA 786
                                                                                                                                                                                                                               133;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0228986
990S-0162866
                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                               55.68;
                                                                                             1324
    region and
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.2;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
    partial
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1656;
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                                                                                                                                                                                                                                                                                                                                                                                                                1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wyatt
                WO200157182-A2
                                             Homo sapiens
                                                                        cytostatic;
                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                 AAK73166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY42648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999
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                                                                                                                                                                                                                                                                                                                      114
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the promoter region and a partial coding region of A. thaliana DZ2AT3 gene.
                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                 Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                   166/c
AAK73166 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1324 BP; 460 A; 214 C; 182 G; 467 T; I other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction shatter resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-580449/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 11; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOG-) BIOGEMMA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AATCGAAGATGGCAACAAAATCCATGGGAGATATCGAGAAAATAAAGAAGAAGAAACTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGAAACTAATCAACGTGTTGATCGTCGATGATGATCATTAAACCGTAGACTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCGAAGATGGCAACAAAATCCACCGGAGGTACCGAGAAAACCAAGTCGATAGAAGTGA 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATG 113
therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; dehiscence; male sterile plant; DZ2AT3;
oilseed rape; response regulator protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitelaw C;
                                                                                                                                                                                                                                                            19965
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Pred. No. 0.001;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                 SEQ
                                                                                 ID NO:27978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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2000US-01354. 2000US-019628. 2000US-019628. 2000US-0186574. 2000US-018866. 2000US-0189123. 2000US-0199123. 200
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-OCT-2000; 20-OCT-2000; 21-OCT-2000; 21-OCT-2000; 21-OCT-2000; 20-OCT-2000; 20-OC
2000US-0236368 2000US-0236369 2000US-0236370 2000US-0237037 2000US-0237037 2000US-0237039 2000US-02349960 2000US-0241809 2000US-0241809 2000US-0244617 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0249210 2000US-0249211 200US-0249211 2000US-0249211 200US-0249211 200US-0249211 200US-0249211 200US-0249211 200US-0249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic contivity, and can be used in gene therapy and vaccine production. (1) controlled and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (1) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) concers and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic arityen genomic concers and cancer metastases of haematopoietic arityen genomic concers from the present invention. AAK54942 to AAK84950 and AAM82169 concers sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 90
  15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                          graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell cycle; human; CpG dinucleotide; cytosine methylation, human immunodeficiency virus; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS45453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS45453 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK54951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                    15~MAR-2001;
                                                                                                                                                                                           20-SEP-2001
                                                                                                                                                                                                                                              WO200168911-A2
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemically pretreated complementary DNA associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19965
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                                                                                                                                                                                                                                                                                                                                                      primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                    2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 4699 A; 5296 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%;
54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27978; 3071pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45.6; DB Pred. No. 0.022; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5505 G; 4465 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cycle #79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Matches
                                           Query Match
Best Local
                                                                                                                                                                                                                                           DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HTV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated by the property of the property of the pretreated by the property of the property of the pretreated by the property of the pretreated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with cell cycle
                                                                                                                                                                     Sequence 9515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 158; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-)
        109;
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
        Conservative
                                                                                                                                                                     2719 A; 220 C; 1904 G; 4672 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG
                                       7.5%;
50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin
    0;
                                           Score 45.4; DB Pred. No. 0.019;
    Mismatches
    106;
                                                                                  22;
    Indels
                                                                              Length
                                                                                       9515;
0
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    Gaps
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AAK89374 standard; AAK89374; DNA; 32206 ВP

В δÃ B δõ

4785

495

В δÃ

4665

375 AACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCATGGATGCTTGATGGA 434

0

AAGTTTTAGTAAAGAGAAAAAATATTATTGTATATATAGGAGTTAGATGTAATTTATAGA 4724

4725

435

δÃ

555

4845 TAGGGTGATTAATATATATATATATTTTATAATT 4879

TAAGTTGTTGCTTTAAGCTTATAAAATATTTAAAT

TACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATAATCATG

554 4784

RESULT 13 AAK89374/c Human; digestive system antigen; gene therapy; cancer, ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds. Human 05-NOV-2001 digestive (first entry) system antigen genomic sequence SEQ Ħ

appendicitis; chronic colit

colitis;

NO:

2950.

02-AUG-2001

WO200155314-A2

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31-JAN-2000
24-FEB-2000
24-FEB-2000
10-MAR-2000
11-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0179065.
2000US-018628.
2000US-0188628.
2000US-0188674.
2000US-0198123.
2000US-0199076.
2000US-01991135.
2000US-0211647.
2000US-0211647.
2000US-02116488.
2000US-0216488.
2000US-0212688.
2000US-0212513.
2000US-0212513.
2000US-0225114.
2000US-02252513.
2000US-02252513.
2000US-0225257.
2000US-0225257.
2000US-0225257.
2000US-0225257.
2000US-0225447.
2000US-0225477.
2000US-0225477.
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2000US-0225688.
2000US-0225688.
2000US-022589244.
2000US-022589244.
2000US-022589244.
2000US-022589244.
2000US-0229345.
2000US-0229513.
2000US-0229513.
2000US-0239437.
2000US-0231243.
2000US-0231244.
2000US-0231414.
2000US-0231968.
2000US-0233981.
2000US-023399.
2000US-023399.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233403.
2000US-02344274.
2000US-0234937.
2000US-0234937.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
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  17 NOV 2000
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02-CCT-2000
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03-CCT-2000
03-CCT-2000
03-CCT-2000
03-CCT-2000
03-NOV-2000
03-NOV
  Polynucleotides encoding digestive system antigens, useful for
                                                                                                                         ( HUMA - )
                                           2001-502630/55
                                                                             CA,
                                                                                                                         HUMAN
                                                                                                                                                             2000US-0236370
2000US-02376370
2000US-0237038
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0239935
2000US-0241921
2000US-0241808
2000US-0241808
2000US-024181808
2000US-0246477
2000US-0246477
2000US-0246477
2000US-0246477
2000US-0246477
2000US-0246528
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249218
2000US-0251988
2000US-0251869
2000US-0251869
2000US-0251869
2000US-0251869
                                                                                                                         GENOME
                                                                                SC,
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RESULT 14
AAV83939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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Best Local S
Matches 91
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               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis ulcerative colitis. The present sequence is a genomic DNA fragment
                                                                               New isolated nucleic acid comprising neocentromere sequences eukaryotic chromosome - used to produce replicable, segregati artificial chromosomes that can carry large amounts of DNA for
                                                                                                                                                                                                                                                                                                                                                                 neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
THE present sequence represents the chromosome 10, 10q25.2 region. This
                                                                                                                                                                                                                    26-AUG-1997;
13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                      HC-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases \cdot
                                        Claim 8; Fig 6; 540pp; English
                                                                                                                                       WPI; 1999-009773/01.
                                                                                                                                                                 Cancilla MR,
                                                                                                                                                                                                                                                             13-MAY-1998;
                                                                                                                                                                                                                                                                                                                WO9851790-A1
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV83939 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32206 BP; 9503 A; 5480 C; 7017 G; 10206 T; 0 other;
                                                                                                                                                                                         (AMRA-) AMRAD
                                                                                                                                                                                                                                                                                        19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATGTGTATATGTGTATATATGTGTATATGTATATATACGTGT 22034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from normal human chromosome 10q25.2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2950; 986pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                         OPERATIONS PTY LTD
                                                                                                                                                               Choo K,
                                                                                                                                                                                                                   97AU-0008791.
97AU-0006784.
                                                                                                                                                                                                                                                             98WO-AU00352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%;
54.2%;
                                                                                                                                                                 Du Sart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                 Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
  HC-contig derived from normal human region can be naturally mutated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 32206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                 segregating of DNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 15
AAK76447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC produce an unusual chromosomal marker referred to as mardel(10) The CC mardel(10) marker is mitotically stable and contains a functional CC neocentromere at a location regarded as non-centromeric. This cc neocentromere maps to q25.2 on chromosome 10. The specification describes CC nucleic acid sequences derived from a cukaryotic chromosome, including a CC neocentromere or its functional derivative or hybrid, that are able, in CC a compatible cell, of replicating, acting as extra-chromosomal element CC construct artificial chromosomes for use in gene therapy comprising a CC replicable, segregating nucleic acid that confers a specific phenotype CC on cells. Human artificial chromosomes can propagate in human cells and CC carry large amounts of DNA (e.g. therapeutic genes), and, being CC extra-chromosomal, they are not mutagenic. The artificial chromosomes CC are also useful for generation of transgenic plants and animals, in CC production of proteins and to make diagnostic reagents, e.g. for CC expression of cytokines, receptors and growth factors, or to increase CC the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
18-APR-2000;
19-MAY-2000;
19-MAY-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15708 ATATGTATATATGTGTATATAGACATAAATATGTATATGTGTATAT 15755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15588
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                                                                                                                                                                                               31-JAN-2000;
                                                                                                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                               cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                Human; immune;
                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK76447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                     WO200157182-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80595 BP;
                            2000US-0214886.
2000US-0215135.
2000US-0216647.
                                                                       2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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                                                                                                                                                  2000US-0184664
2000US-0186350
                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                       2000US-0189874
                                                                                                                                                                                  2000US-0180628
                                                                                                                                                                                               2000US-0179065
                                                                                                                                                                                                                                                                                                                                                               haematopoietic;
                                                                                                                                                                                                                                                                                                                                               therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 4445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23183 A;
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54.28;
                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                               immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23975 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 31259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597
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2000US-0217496.
2000US-0218290.
2000US-0220963.
    2000US -0230437

2000US -0231242

2000US -0231243

2000US -0231241

2000US -0231414

2000US -0231414

2000US -0232081

2000US -023239

2000US -023239

2000US -023239

2000US -023239

2000US -023239

2000US -023239

2000US -023240

2000US -023240

2000US -023240

2000US -0233063

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2000US -023427

2000US -023427

2000US -0235484

2000US -0235484

2000US -0235836

2000US -0236367

2000US -0236367

2000US -023637

2000US -0237037

2000US -0237037

2000US -02341785

2000US -0241786

2000US -02411808

2000US -0241808

2000US -0241808
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2000US-0227924

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2000US-0229345
        01-NOV-2000
08-NOV-2000
017-NOV-2000
017-
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in each therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic useful for preventing, diagnosing and/or treating metastasis
                                                                                                                                                                                                                                                                                metastasis
                                                                                                                                                                                                                                                                                                                                                           2001-483426/52.
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2000US-02446474
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2000US-0249201
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2000US-0251988
2000US-0251989
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cancers
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14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 20-OCT-2000 20-OC

14-AUG-2000 12-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 01-SEP-2000 01-SEP-2000

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Search completed: November 7, 2002, 12:30:12 Tob time: 291 secs
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                                                                                                                                                                                                                                                                                                                          Query Match 7.3%; Score 44; DB 22; Length 4445; Best Local Similarity 58.3%; Pred. No. 0.035; Matches 77; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4445 BP; 1164 A; 1222 C; 1054 G; 1005 T; 0 other;
                                                                                                                                                                                                                                         399 TCCCTCTCATTAACCAACTCATGGATGCTTGATGGATATATTTTATATTTATGGAAACA 458
                                                                               737 TATATATTTTT 748
                                                                                                                      519 TTTAGGGTTCTT 530
                                                                                                                                                          677 CACATATACACATATATGCGTATATATATATATATATACGTATATGTGTATATGTATA 736
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nucleic search, using
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq: *
/cgn2_6/ptodata/1/ina/6A_COMB.seq: *
/cgn2_6/ptodata/1/ina/6B_COMB.seq: *
/cgn2_6/ptodata/1/ina/backfiles1.seq: *
/cgn2_6/ptodata/1/ina/backfiles1.seq: *
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US-08-464-105-7
US-08-484-106-7
US-08-136-7438-3
US-08-771-784-1
US-09-076-756-1
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US-09-076-756-1
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US-09-078-294-4
US-09-381-862-3
US-08-486-013-70
US-08-482-279-70
US-08-382-279-70
US-09-015-968-70
US-09-015-968-70
US-09-078-964-4
US-09-286-799-1
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(without alignments)
3161.878 Million cell updates/sec
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Compugen Ltd
          Sequence 63, Appli
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Sequence 24, Appli
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 Sequence
RESULT 2
US-08-232-463-14/c
US-08-232-463-14/c
; Sequence 14, Application US/08
; Patent No. 5670367
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMB
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US-09-228-986-63
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 1100//1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
SEQ ID NO 63
LENGTH: 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728
                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                          611 TTAATCTTTACTGTGAAGAAGCTGAGAATGGGAAAGTAGCAGTGGACTATTTCAAGCAGG
                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                                                                                                                                                551 TCTTGCTCGTGGAAGACACACAAATCAACAGAATAATTTTCGGGAAGGGTGCTTCAAAGCC 610
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                                                                                                                                                                            CGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCA 310
                                                                                                                                                                                                                                    GCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAGAGGGATGGTGTTT 251
                                                                                                                                                           AGGCAACAAGGCAACTGAGATCAATGGGAGTCAAGACACCCATTGTTGCACTTACAGCA
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33; Conservative
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   RECOMBINANT FOWLPOX VIRUS
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US-08-447-500-1
US-08-447-4097-1
US-08-447-408-1
US-08-453-866-1
US-08-453-866-1
US-08-185-359-1
US-08-560-022-11
US-08-560-022-11
US-08-960-022-11
US-08-960-0240-1

    Mismatches

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Pred. No. 1
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Title: Perfect score:

Scoring table:

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NUMBER OF SEQUENCES:

52

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, CLUNE: PTZ9Pt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 29,768
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
TELEX: 899149
                                                                                                           1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1000
CITY: Alexandria
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                        361
                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                 241 GGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 8.9%; Score 54; DB Local Similarity 7.5%; Pred. No. 3.1e-
les 33; Conservative 220; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGCACGAGCAGAATCGAAGATGGCAACAAATCCATGGGAGATATCGAGAAAATAAAGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                            CCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGCTTGATGGATATA 438
                                                              CCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACTCAT 420
                                                                                                       CATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAATCAT 180
                                 GGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Nucleotide sequence of HC-contig US-09-078-294-3
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                                                                                                                                                                                                                                ; ORGANISM: Nucleotide sequence of NC-contig US-09-078-294-4
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US-09-078-294-3
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                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION (NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09078294 Patent No. 6265211 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09078294 Patent No. 6265211
                                                                                                                                                      Matches
                                                                                                                                                                     Query Match 7.3%;
Best Local Similarity 54.3%;
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Best Local :
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                         15605 ATAAATATGTATATGTGTATATAGACATAAATATGTATATATGTGTATATAGACATAA 15664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15648 ATAAATATGTATATATGTGTATATAGACATAAATATGTATATATGTGTATATAGACATAA 15707
15665 ATATGTATATATGTGTATATAGACATAAATATGTGTATATAGTGTATATAGACATAAATAT 15724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15708 ATATGTATATATGTGTATATAGACATAAATATGTATATGTGTATAT 15755
                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                     LENGTH: 80246
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                                                                                               490 ATAGATACTIGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 TCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 54.2%;
                              ATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAATCAT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
                                                                                                                                                      89;
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                                                                                                                                                      Conservative
                                                                                                                                                    0;
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                                                                                                                                                  Score 44; DB 4; Le
Pred. No. 0.0063;
0; Mismatches 75;
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Pred. No. 0.0037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77;
                                                                                                                                                                                         Length 80246;
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                                                                                                                                                    Indels
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US-09-381-862-3
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US-09-381-862-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 170; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAI-ENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/381,862
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
TD 1007-770N NUMBER: US/097-71077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 19036/36274 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 1997-71077

FILING DATE: 25-MAR 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP98/01288

FILING DATE: 23-MAR-1998

ATTORNEY/AGENT INFORMATION:

NAME: /// COLUMN TO THE PRIOR A POLICY TO TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS TITLE OF INVENTION: CAUSED BY STREETCOCCCUS PYOGENES NUMBER OF SECTIONS
2814 GGACGTGAAGGGGTTGATTTGGCATTGGCTTTGAAGCCAGATGTTTTGGTTATGGATCTA 2755
                                                                                                                                                     2874 GGACTCAAGAGTTTTTTGAATTTACAAGCTGATATTGATGTCGTTGGTGAGGCCTCTAAT
                                                                                                                                                                                                                                                                                                              2934 GAGATGACGATGAGTAAGATAAAAGTGATATTGGTCGATGATCATGAAATGGTCCGCATG 2875
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                                                                                                                                                                                                                               554 GTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                     47 GAGAAAATAAAGAAGAAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
STRAIN: Clinical Isolate SP-14-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cawley, Jr., Thomas A. REGISTRATION NUMBER: 40,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                          GAGGCAGTAATCATCCACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5014 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%;
ilarity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abe, Kanako
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Length 5014;
Pred. No. 0.031;
0; Mismatches 195; Indels
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RESULT 6
US-08-486-013-70
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Patent No. 5731149
GENERAL INFORMATION:
Query Match 6.6%;
Best Local Similarity 45.6%;
Matches 140; Conservative
                                                                                                                                                                                                TELEFAX: (619) 535-894 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-NOV-19
APPLICATION NUMBER: US
                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE_DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2637
                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2694 GCTAAGGTACTTGTGTTAACTTCCTATCTAGATAATGAAAAGATATACC---CTGTCATT 2638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antibiotic Cryptdin Peptides and TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2754 GTGATGCCAGAGTTAGGCGGTGTTGAGGCAACTTTAGAAGTTCTAAAAAAATGGAAAGAG 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGCAGGAGCGAAGGGTTATATGTTAAAAACATCGAGTGCGGCTGAAATTTTAAATGCC 2578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATGCCCGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                         2551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouellette, Andre J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                       single
                                                                                                                                                                                                                   535-8949
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                                                                                                                                                                                                                                                                                                                                                                           us 07/889,020
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                                                                                                                                                                                                                                                                                                                                                                                                                                  07/930,649
      0;
                                                                                                                                                                                                                                                                            P-UC 1206
    Score 39.8; DB 1;
Pred. No. 0.027;
0; Mismatches 167;
                                       Length 2551;
      Indels
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298 TGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACT 357

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US-08-482-279-70
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 70,
                                                                                                                       TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Selste
APPLICANT: Ouelle
                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                 FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA: 27/889,020
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-NAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and
TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 CACTTAC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITHE READABLE FLOPPY disk
MEDITH TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
                                                                       STRANDEDNESS:
                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/342,268 FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                     nucleic acid
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California
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4370 La Jolla Village Drive, Suite
                                                                                                        2551 base pairs
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                                                        linear
 6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/482,279
                                                                                                                                                                                                                  P-UC 1206
Score 39.8;
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DB
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2;
Length 2551;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: 92122
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYPEN: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5844072
GENERAL INFORMATION:
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                                                                                                                                                      APPLICATION NUMBER: US/08/342
FILING DATE: 18 NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA: 07/889
PRIOR APPLICATION NUMBER: US 07/889
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A.
REGEISTRATION NUMBER: 9-IIC
REGISTRATION NUMBER: 9-IIC
                                                                          TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                           REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbel:
STREET: 4370 La Jo.
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
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                                                                                                           TELEPHONE:
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   STRANDEDNESS:
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               H: 2551 base pairs
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4370 La Jolla Village Drive, Suite 700
                                                                                        (619) 535-9001
(619) 535-9001
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single
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0; Mismatches 1
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                                                                                                                                                             FILING DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/482,279
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
US 08/342,268
APPLICATION DATA:
18-NOV-1994
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Best Local Sim
Matches 140;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 14-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7'CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                                   FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 TGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACT 357
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                  NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                          APPLICATION NUMBER:
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40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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4370 La Jolla Village Drive, Suite
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                                                                           26-MAY-1992
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NUMBER:
                                                                                                                                                 US 07/930,649
                                                                                            US 07/889,020
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P-UC 3003
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Best Local s
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INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 2551 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
            APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 GTGTATGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 TGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 TAACCATTGCTTGGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACT
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                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
APPLICATION NUMBER:
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                           California
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4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                           USA
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                                               US 08/482,279
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US 08/342,268
                                                                                US/09/015,968
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Pred. No. 0
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0.027;
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18-NOV-1994

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; ORGANISM: Drosophila virilis US-09-031-563-26
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US-09-031-563-26
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FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UC

TELECOMUNICATION INFORMATION:

TELEPHONE: (619) 53-9001

FELEPAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 2551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-397-386-70
                                                                                                                             SEQ ID NO 26
LENGTH: 4586
                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09031563A Patent No. 6022708
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.6%;
Best Local Similarity 45.6%;
Matches 140; Conservative
     Best Local Similarity Matches 89; Conser
                                        Query Match
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/031,563A
CURRENT FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                      APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: FUSEd
FILE REFERENCE: P1272
                                                                                                              TYPE: DNA
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                          303 CACTTAC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AGTATATATGTTTTATATATATATATATATATATGTATATGTATATATATATATGTGTGTGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 CATGGATGCTTGATGGATATATTTTATATTATGGAAACACACATAATAACGTCTAAGT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 IGGGGTGACTICACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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     Conservative
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26-MAY-1992
                   52.0%;
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 Score 39.8; DB 3;
Pred. No. 0.034;
0; Mismatches 82;
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Pred. No. 0.027;
0; Mismatches 167;
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                                    Length 4586;
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Gaps
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; TYPE: DNA
; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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US-09-078-294-3/c
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US-09-078-294-4/c
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                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Destree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 3
                                  Query Match
                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09078294 Patent No. 6265211
 Best Local Similarity Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                             15306 GTGTGTATATGTACATACATACATACATAAATA 15270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15366 ATACATATTTATGTCTATATACACATATATACATATTTATGTATATTTATGTATATATTTATGTATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Nucleotide sequence of NC-contig
                                                                                                                     LENGTH: 80595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 ATACTTGCATGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATATAATCAT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487
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 Conservative
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                  6.48;
52.98;
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Pred. No. 0.23
0; Mismatches
                  Score 38.6; DB Pred. No. 0.23;
 Mismatches
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 74;
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                                Length 80595;
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US-08-629-643A-5
                                                                                               Query Match
Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                               2563 CTGCATATATATATATATATATATATATATATATATATGTGTGTGTGTGTGTGTGTGT 2622
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                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/629,643 FILING DATE: 09-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/629,643A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, N. A. TITLE OF INVENTION: I
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 486 ATGCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTAT 533
                                                              426 CTTGATGGATATATTTTATATTATGGAAACACACATAATAACGTCTAAGTGTGTATGT 485
                                                                                                                                                                               NAME/KEY: mat_peptide
LOCATIO: 650...371
OTHER INFORMATION: Join 650..730, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-359-3263
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Search completed: November Job time: 293 secs
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-280-799-1
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APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: MCKAY, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
TITLE OF INVENTION: TRANSDUCTION
FILE REFERENCE: ISPH-0340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09280799 Patent No. 6136603
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 208
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CURRENT FILING DATE: 1999-03-26
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BM373897 EBma03_SQ
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AQ488569 RPCI-11-2
BM358320 EBed01_SQ
BM415113 OP20184 M
AL222093 Tetraodon
AL106171 Drosophil
AZ301735 GM_UMD01
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ALIGNMENTS

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ASTORNAL STORE MAKE A LINEAR EST 02-DEC-2001
DEFINITION

STOREM CONTROL OF MAKE A CLONE GENOME SYSTEMS CLONE ID:

Gm-c1019-4294 5' similar to TR:082445 082445 RESPONSE REGULATOR

PROTEIN .' mRNA sequence.

ACCESSION

AWZ/8862.1 GI:6667411

EST.

SOURCE

SOURCE

ORGANISM
EMALYOSTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

ROSIDAE; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

REFERENCE

1 (bases 1 to 376)
AJFORNAL .' Person, B. Marra, M. Hiller, L., Erpelding, J., Coryell, V. Khanna, A., Bolla, B. Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C.,

Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

'Y. Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schutz, K., N., Schutz, R., Waterston, R., and Wilson, R., Pape, D., Harvey, M., Schutz, R., R., Waterston, R., and Wilson, R., Pape, D., Harvey, M., Schutz, R., R., Waterston, R. and Wilson, R.

TITLE

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810

Fax: 314 286

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62 AAACTAAACGTGTTGATCGTCGATGATGATCCACTAAACCTTATAATTCATGAGAAGATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGAGAGTGTTGGAATGAAAATCAAGGAGTGGAAAATGGCCAAGAAGCAGTGGACATT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCAAAGCGATTGGGGGTATTTCACAGACAGCGAATAACGGTGAGGAGGCAGTAATCATC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTACCATGAGAAACCCTTGAACAATTCTAAGCTTAGTTCACTTCTTGATAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTTGGG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCGTGACGGCGGCTCATCTTTTGACCTTATCCTAATGGATAAAGAAATGCCCGAGAGG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATCATCACGCTGT----ACGGAAGCAGAAATACGAAAATTTATGGAAGCGGGACTGAAT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGACTTCACTGGCTGACAATGAAGAGGAGCGCAGGGCTTTCATGGAAGCTGGACTTAAC 361
Vodkin,L., Keim,F., Shoemaker,R., Retzel,E., Khanna,A., Carpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565) Unpublished (1999)
Other_ESTs: AW278862 corresponding to Gm-c1019-4294 (5') Contact: Vodkin, L.O., PI, A Functional Genomics Program
                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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BE822715
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                                                                                                                                                                   (bases 1 to 568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pspORT1 (Life Technologies); Site_1: Not I; Site_2: Sal I; This cDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (d7) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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Pred. No. 9.5e-08;
0; Mismatches 156;
                                                                             Retzel,E., Khanna,A., Coryell,V
Pardinas,J., Liu,L. and Lewin,H.
Soybean (NSF 9872565)
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                                                                                                                                        Coryell, V.
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                                                                                                                                                                                                          GAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCACTGGCTGACAATGAAGAGG
                                                       AAATACGAAAATTTATGGAAGCGGGACTGAATGACTACCATGAGAAACCCTTGAACAATT
                                                                                                         AGCGCAGGGCTTTCATGGAAGCTGGACTTAACCATTGCTTGGCAAAACCGTTAACCAAGG
                                                                                                                                                              GCTCAATGGGCATTGGTAGCATGATTGTTGGTGTATCATCACGCTGT---ACGGAAGCAG
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26

Matches

BASE COUNT ORIGIN

δÃ 밁 VQ В ρ В QΥ В Qy B

263

203

146 182 80

320

COMMENT

274 389 334 329

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TITLE AUTHORS REFERENCE

SOURCE ORGANISM

KEYWORDS VERSION

ACCESSION DEFINITION RESULT 2 BE822715/c

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Query Match
Best Local Similarity
                                                                                                                                                                                            150 CAGCGAATAACGGTGAGGAGGCAGTAATCATCCACCGTGACGGCGGCTCATCTTTTGACC
                                                                                                                                                                                                                                                                                                                             90 ATCCACTARACCTTATAATTCATGAGAAGATCATCARAGCGATTGGGGGGTATTTCACAGA 149
                                                                  TTATCCTAATGGATAAAGAAATGCCCGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAA
                                                                                                                                 GAGTNGAAAATGGCCAAGAAGCAGTGGACATTCA---TTGCCATNGACAAAGATTTGACC
                                                                                                                                                                                                                                                              ATAAAATCNNNNGAAAGATTCATCAAAAGCTGTTGGAGAGTGTTGGAATGAAAAATCAAG
TGATTCTCATGGACATGGATATGCCCCATCATGAATGGCATTGAGGCAACAAAGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                       175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edwin R. Madigan Building, 1201 W. Gregory, Urbana, Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ystems.com web site:www.genomesystems.com
Seq primer: 5'-TTTTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_ilb="Gm ri070"
/clone="The library Gm-ri070 is a sequence-driven, reracked set of 9.216 clones stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-ri070. The cDNA clones of the reracked Gm-ri070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html. Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Ilinois, http://www.life.uiuc.edu/blotech/keck.html. Note: The Corresponding 5' rem from each lone in the Gm-ri070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         information on the source library for each clone can all be obtained by referring to the Genome Systems clone ID the original cDNA library that is also listed under 'OTHER EST'."

3 110 c 95 g 179 t 21 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The deta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%;
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Pred. No. 7.8e-05;
0; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., 1, Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton, R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On Jul 26, 2000 this sequence version replaced gi:13189622.
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HVSMED0095H05f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEb0095H05f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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     109
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Location/Qualifiers
                                                                                                                                                                                                 /notes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; /notes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; /lotes "Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chol)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Cates, Rambo, Main). The sequence as been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or sequence analysis see
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
barley wheat.pw.usda.gov/ggpages/bgn/31/cover.html)
133 c 182 g
                                                                                                                 sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order

http://www.genome.clemson.edu/orders Also

this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
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Matches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCGGGCTTGCGTAGCGGCCAT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTGGGGTGACTTCACTGGCTGACAATGAAGAGGAGCGCCAGGGCCTTTCATGGAAGCTGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGAGGGATGGTGTTTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGAT 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE602512 732 bp mRNA linear EST 22-OCT-2001
HVSMEh0099H16f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099H16f.
                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                   On Aug 21, 2000 t
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
                                                                                                                                                                                                       Email: rwing@clemson.edu
Total hq bases = 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
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Similarity 49.6%;
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                                                                                                                                                      primer: AATTAACCCTCACTAAAGGG
h quality sequence stop: 687.
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Location/Qualifiers
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                      /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0099H16f"
                                                                            /organism≔"Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                         this sequence version replaced gi:13190328
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Poaceae; Pooideae

EST 22-OCT-2001

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                                                                                                                                                                                                                                                                                                                                                                                     AGCCGACGACTTCACGCCCAAGCCGCTGACCAAGGAGAAGCTGGGCAACATTCTCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189;
                                                  BM373897 426 bp mRNA EBma03_SQ003_A24_R IGF Barley EBma03 libiclone EBma03_SQ003_A24 5', mRNA sequence BM373897
                          вм373897.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 49.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) 177 c 226 g 147 t 27 others
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http://www.genome.clemson.edu/projects/barley.
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/lab_host="SOLR"
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HVcDNA0009 (5 to 45 DAP)"
                       GI:18117287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTCACTG 313
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Pterygota; ; Apoidea;
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BI509132.1
                                                                                                                                                       BI509132 266 bp mRNA linear EST BB170013B10E07 Bee Brain Normalized/Subtracted Library, mellifera cDNA clone BB170013B10E07 5', mRNA sequence.
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Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
                                       Apis mellifera
Eukaryota; Met
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Scottish Crop Research
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Hordeum vulgare
                                                                           honeybee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 00 44 1382 562731 Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Waugh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from maternal tissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

Gene Function) project."

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/clone="EBma03_SQ003_A24"
/clone=1ib="IGF Barley EBma03 library"
/clone_1ib="IGF Barley EBma03 library"
/tissue_type="Maternal tissue"
/dev_stage="8 days post anthesis"
/lab_host="UH10B"
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata
Apidae; Apis.
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                                                                                                                                                                                         CCGTGATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATA 590
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RPCI-11-243N4.TJ I
DNA sequence.
AQ488569
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Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Behavior in the Honey Bee Unpublished (2001)
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Whitfield,C.W., Soares,B.,
Smoller,D. and Robinson,G.E
An Expressed Sequence Tag F
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BACKWARD: ATTAACCCTCACTAAAG
INsert Length: 266 Std Erro
Plate: BB170013B10 row: E co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F. Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="BB170013B10E07"
/clone_lib="Bee Brain Normalized/Subtracted
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/db_xref="taxon:7460"
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/strain="mixed strains of
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54.6%;
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Pred. No. 0.37;
D; Mismatches 79;
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Other_GSSs: RPCI-11-243N4.TV
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                               EBed01_SQ002_N02_R IGF Barley EBed01 libstication EBed01_SQ002_N02 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD
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1 (bases 1 to 696)
Zhao, S., Adams, M.D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Class: BAC ends
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/note="Vector: pBACe3.6; Site_1:
RPCIII Human Male BAC Library"
93 c 106 g 260 t
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/clone="RPCI-11-243N4"
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/db_xref="GDB:7593243"
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Pred. No. 0.45
0; Mismatches
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Invergowrie, Dundee, DD2
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                  1 (bases 1 to 1745)
Heer.J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opp Mixed Stage EST's from Globodera pallida, the potato Unpublished (2001)
Contact: Opperman, C
Center for the Biology of Nematode Parasitism
                                                                                                                        Globodera pallida.
Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                                                                                                                        1745 bp mRNA linear EST 28-JI OP20184 Mixed Stage EST's from Globodera pallida, the potato nematode Globodera pallida cDNA, mRNA sequence BM415113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwaugh@scri.sari.ac.uk
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nter for the Biology of Nematode Parasitism State University; IACR-Rothamsted
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/clone="ib="10F Barley EBed01 library"
/tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
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54.6%;
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Pred. No. 0.49
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ day This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
184002 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                              Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis.
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GT11-11pcN_R_H05_GT11-11_R_044.ab1
Locatlon/Qualifiers
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Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                                                                                       Genoscope.
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/note="Vector: lambda GTl1; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GTl1 by Paul Burroughs,
IACR-Rothamsted."

1ACR-Rothamsted."

25 others
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as part of a large
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                                                                                                                                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr )
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:99883"
/clone="184002"
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/clone_11b="G"
/note="Genoscope sequence ID : COA
/note="10 c 174 g 333 t 101
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/plasmid="pBeloBAC11"
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Penuela,S., Larson,K., M
Foster-Hartnett,D. and Y
BAC end sequences from s
analogs (RGAs)
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                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Young Nevin D
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                              Seq primer: M13F
Class: BAC ends.
                                                                                                                                                                                                                                       495 Borlaug Hall, 1991 Upper Buford
Tel: 612 625 2225
Fax: 612 625 9728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          max genomic, DNA sequence. AZ301735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ301735.1 GI:9886509
                                                                                                                                                                                              NBSDH8
                                                                                                                                                                                                            Sequence on contig
                                                                                                                                                                                                         neviny@tc.umn.edu
se on contig Gm_NBSDH8_ctg_b near
                                          /clone_lib="Glycine max resistance gene analogs (pECSBAC4 ECORI)"
/tissue_type="cotyledon leaves"
/dev_stage="cotyledon stage"
/note="Vector: pECSBAC4; Site_1
                                                                                       /organism="Glycine max"
/cultivar="Faribault"
/db_xref="taxon:3847"
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Mudge, J., Danesh, D., Denny, R., Young, N.D.
                                                                                                                                                                                                                                                                                                                                                              soybean
 stage"
C4; Site_1:
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from UMN
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                                                                            clones
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[) Glycine
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RESULT 13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 TGATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATTTAAATAAGGGTTT 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae, Musidae, Musidae; Muridae; Muridae; Musidae; Mamil, C., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0503 row: E column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ640886 541 bp DNA linear GSS 14 1M0503E11F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0503E11 F, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CGTTGTAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ640886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ640886.1 GI:11764326
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0503E11"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                          /sex="Male"
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50.0%;
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ORGANISM
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AZ009832/c
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VERSION
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Best Local Sir
Matches 120;
                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 GTTCTTTATCGTCCGTGATATATAATCATGTAAGTTGTTGCTTTAAGCTTATAAAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 TGGGAGTTAGTGAATNTGCTTGCTTGTCTTTGGCTCTTACAAGTAGCATTTTCAACTAGA 444
                                                               Unpublished (1999)
Other_GSSs: RPDI-23-324H4.TV
Other_GSSs: RPDI-23-324H4.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MT
Tel: 301 838 0208
Fax: 301 838 0208
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and Fraser,C.M.
Mouse BAC End So
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 to 610; Chases 1 to 610; Chases, Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ009832
AZ009832.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ009832 610 bp DNA Linear RPCI-23-324H4.TJ RPCI-23 Mus musculus genomic clone
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong
                                                   Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                    Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance. "
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Pred. No. 1
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                                                                                                                                                                                                                                                        Library RPCI-23
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                                                                                                                     20850, USA
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RPCI-23-324H4,
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RESULT 15
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ORIGIN
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                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 ATATATATATGCT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 GCATAGATACTTGCATGTGTGTGTTTTAGAATTTAGGGTTCTTTATCGTCCGTGATATAT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCATGTAAGTT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 853)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGIH80TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BH516724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH516724 853 bp DNA linear GSS 13-DEC-2001 BOGIH80TR BOGI Brassica oleracea genomic clone BOGIH80, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). 3AC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 324 row: H column: 4
Seg primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
                                                                                             Seq primer: TR
Class: sheared ends
                                                                                                                           Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq_primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea.
Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH516724.1 GI:17724814
                                                                                                                                                                                                                                                   Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                 Medical Center Drive, Rockville, 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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//ab_host="DHIOB"
//ab_host="DHIOB"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: panchey and/or
// note="Organ: Kidney/Brain; Vector: panchey and/or
// partially digested
// with a combination of EcoRI and EcoRI methylase. Size
// selected DNA was cloned into the pBACe3.6 vector at the
// selected DNA was cloned into the pBACe3.6 vector at the
// partially digested
// 
                                 Location/Qualifiers
1. .853
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/clone="RPCI-23-324H4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.48;
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                                                                                                                                                                     provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
1.7;
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                                                                                                                                                                            Tom
                                                                                                                                                                                                                                                                                                                   USA.
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                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                Query Match
Best Local
417 AGAGAAACCTCTCACCATCTCTAAACTTGTCTCTATTCTTCATAATCT 370
                                   370
                                                                     474 TAGAGCTGAGGAAGAAGAGGTG---AAAGAGTTTATGGAAGCTGGACTTAATGACTTTCA 418
                                                                                            310 ACTGGCTGACAATGAAGAGGGGCGCAGGGGCTTTCATGGAAGCTGGACTTAACCATTGCTT 369
                                                                                                                                           534 TTAGGCGACAAGGAGACTAAGAGAGATGGGGGATAGAGAGCAAGATAGCAAGGAGTAACAAC 475
                                                                                                                                                                             250 TTCGACAACTAAGAAGCTAAGAGAAATGGAAGTGAAGTCAATGATTGTTGGGGTGACTTC 309
                                 GGCAAAACCGTTAACCAAGGACAAGATCATCCCTCTCATTAACCAACT 417
                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                        268 a
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                    /strain="TO1000DH3"
/db_xref="taxon:3712"
/dlone="BOGIHB0"
/clone=lib="BOGI"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
a 154 c 145 g 286 t
                                                                                                                                                                                                                                7.48;
                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                Score 44.8;
Pred. No. 1
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                .0
                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                 67;
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Search completed: November Job time: 1705 secs 7, 2002, 14:25:27